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Title: Genetic algorithm for nuclear data evaluation

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Genetic algorithm for nuclear data evaluation

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Initial population

• Normally sample μ , σ using uncertainties around the mean N times

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$$P = \begin{bmatrix} \mu_1, \sigma_1 \\ \mu_2, \sigma_2 \\ ... \\ \mu_N, \sigma_N \end{bmatrix}$$

- Each row of P is a member in the population
 - There are N members total in the population

Fitness (outer loop)

- Ideal is fitness=0
- $FF = \sum \frac{C-E}{F}$, summed over all configurations of all experiments
- Each member of the population has a value of FF (fitness function) assigned to it
- Convergence criteria is that min(FF), which is associated with the most fit member of the population, stops changing more than a certain amount (i.e., 1%)
 - This means that the fittest member of the population is not getting much more fit from generation to generation

Calculate fitness

- My proposed method:
- Input original (C-E)/E values and original μ , σ values
- Also input sensitivities such as: $\frac{d\left(\frac{C-E}{E}\right)_{R_1}}{d\mu}$
 - These sensitivities are each specific to a single configuration of a single experiment

Selection (1st part of inner loop)

- N times, pick 2 parents and have them reproduce
 - This creates the next generation of N members
 - There is no limit to how many times a single member can be a parent
- Pick random # between min(FF) and max(FF)
 - I.e., the # can be anywhere from the FF value of the most fit member of the population to the FF value of the least fit member of the population
- 1st 2 members that have FF<=random # are the parents
 - After randomizing population vector of course
- This makes it so that more fit members of the population are more likely to be chosen, but even members with the worst fitness still have a chance to reproduce

Reproduction (2nd part of inner loop)

- Crossover with mutation probability
- Reproduce by averaging the μ and σ values of each of the parent pairs chosen in the selection step
- Each time an average is taking, there is a 1% chance that a random value is picked instead of the average
 - Random value ("mutated" value) is generated the same way the initial population was generated

Solution

 The optimized solution is the member of the population that has the minimum (best) value of FF at the time of convergence of the minimum value of FF

Example

- N=100
- Using real μ, μ unc., σ, σ unc., and (C-E)/E inputs
- Made-up sensitivities (of (C-E)/E values to a change of a single unc.):
 - \circ R₁ to μ : .01
 - \circ R₂ to μ : .001
 - \circ M_I to μ : .001
 - \circ R₁ to σ : .001
 - \circ R₂ to σ : .01
 - \circ M_I to σ :.01

Mutation rate: 10%

Convergence criteria: .1%

Example

- Original FF=1.8144
 - o Original nuclear data: 3.182, 4.098
- New FF=1.2742
 - New nuclear data: 3.1815, 4.0795